mOD K1	TM1	
OKKI	MESPIQIFRGDPGPTCSPSACLLPNSSSW::::::FPNWAESDSNGSVGSEDQQLESAHISPAIPVIITAVY	66
mORD1	ME:::::::::::LVPSARAELQSSPLVNLSDAFPSAGANASGSPGARSASSL:::ALAIAITALY	
mORK1	THE VICE OF THE VITALIAM TATNIYIF NLALADAL VTTTMPFOCA VVT MYCYTH TO THE CONTROL OF THE CONTROL O	138
mORD1	SAVCAVGLIGNVLVMFGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGELLCKAVLSID	
mORK1	YYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKITNICIWIIA	210
	""""""""""""""""""""""""""""""""""""""	
	YYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGAVV::C	
mORK1	SLQFPDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVVAV	200
	TM 6	269
mORK1	FIICWTPIHIFILVEALGSTSHSTAALSSYY: FCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRME	
mORD1	FVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSLNPVLYAFLDENFKRCFRQLCRTPCGRQE	341
mORK1	RQSTNRVRNTVQDP::::ASMRDVGGMNKPV - 380 (SEQ ID NO:2)	
nORD1	PGSLRRPRQATTRERVTACTPSDGPGGGAAA - 372 (SEQ ID NO:4)	



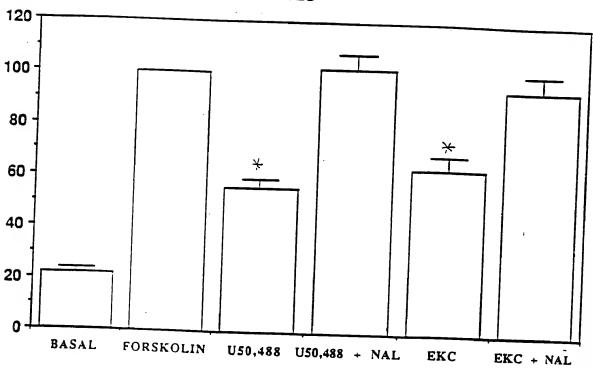
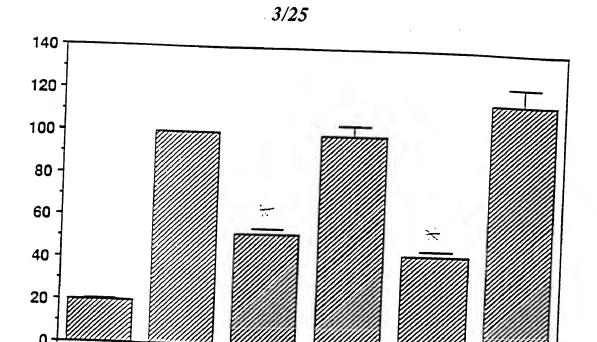


FIG. 2a



DSLET DSLET + NAL DPDPE DPDPE + NAL

FIG. 2b

FORSKOLIN

BASAL

1	AAGAAGCAAAATCAGTAATCCAAAGGCTATCACAAACACATTCACCTTATGGGGTTTGAC
61	TyrThrLysMetLysThrAla TTGAAAATGGAGGGAAATGCTATTGTTTCTTTTTTTTTT
121	ThrasnIleTyrIlePheAsnLeuAlaLeuAlaAspAlaLeuValThrThrHetPro CAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGC
181	PheGlnSerThrValTyrLeuMetAsnSerTrpProPheGlyAspValLeuCysLysIle CCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGA
241	VallleSerlleAspTyrTyrAsnMetPheThrSerllePheThrLeuThrMetMetSer TAGTAATTTCCATTGATTACTACAACATGTTCACCAGCATCTTCACCTTGACCATGATGA
301	ValAspArgTyrIleAlaValCysHisProValLysAlaLeuAspPheArgThrProLeu GCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCT
361	LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerSerValGlyIleSerAla TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTG
421	<pre>IleValLeuGlyGlyThrLysValArgGluA CAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGGT::::::::::</pre>
481	spValAspValIleGluCysCysLeuGlnPheProAsp GGTTTTTATTGCCCTCCTCCAGACGTCGATGTCATTGAGTGCTGCTTGCAGTTCCCAGAT
541	AspAspTyrSerTrpTrpAspLeuPheMetLysIleCysValPheIlePheAlaPheVal GATGACTACTCCTGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTG
601	${\tt IleProValLeuIleIleIleValCysTyrThrLeuMetIleLeuArgLeuLysNNNVal}\\ {\tt ATCCCTGTCCTCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGANNGTC}\\$
661	ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal CGGCTCCTTTCTGGCTCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTC
721	LeuValValAlaValPheValValCysTrpThrProlleHisIlePheIleLeuVal CTGGTGGTGGTGGCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTG
781	GluAlaLeuGlySerThrSerHisSerThrAlaAlaLeuSerSerTyrTyrPheCysIle GAGGCTCTGGGGAGCACCTCCCACAGCACAGCTGCTCTCCCAGCTATTACTTCTGCATC
841	AlaLeuGlyTyrThrAsnSerSerLeuAsnProIleLeuTyrAlaPheLeuAspGluAsn GCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTCTCTACGCCTTTCTTGATGAAAAC
901	PheLysArgCysPheArgAspPheCysPheProLeuLysMetNNNMetGluArgNNNSer TTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGNATGGAGCGCNAGAGC
961	ThrSerArgValArgAsnThrValGlnAspProAlaTyrLeuArgGluIleAspGlyMet ACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATG
1021	MetAsnLysProValop ATGAATAAACCAGTATGACTAGTCGTGGA (SEQ ID NO:12) (SEQ ID NO:11)

Met Glu Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro Thr Cys Ser Pro Ser Ala Cys Leu Leu Pro Asn Ser Ser Trp Phe Pro Asn Trp Ala Glu Ser Asp Ser Asn Gly Ser Val Gly Ser Glu Asp Gln Gln Leu Glu Ser Ala His Ile Ser Pro Ala Ile Pro Val Ile Ile Thr Ala Val Tyr Ser Val Val Phe Val Val Gly Leu Val Gly Asn Ser Leu Val HUMAN Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile MOUSE Met Phe Val Ile Ile Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile HUMAN Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr Met MOUSE Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr Met 100 105 110 HUMAN Pro Phe Gln Ser Thr Val Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp MOUSE Pro Phe Gln Ser Ala Val Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp 115 120 HUMAN Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr MOUSE Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr 135 Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val HUMAN MOUSE Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val 150 Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Leu Lys Ala Lys Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Leu Lys Ala Lys HUMAN MOUSE Ile Ile Asn Ile Cys Ile Trp Leu Leu Ser Ser Ser Val Gly Ile Ser HUMAN Ile Ile Asn Ile Cys Ile Trp Leu Leu Ala Ser Ser Val Gly Ile Ser MOUSE Ala Ile Val Leu Gly Gly Thr Lys Val Arg Glu Asp Val Asp Val Ile Ala Ile Val Leu Gly Gly Thr Lys Val Arg Glu Asp Val Asp Val Ile HUMAN MOUSE Glu Cys Cys Leu Gln Phe Pro Asp Asp Asp Tyr Ser Trp Trp Asp Leu Glu Cys Ser Leu Gln Phe Pro Asp Asp Glu Tyr Ser Trp Trp Asp Leu HUMAN MOUSE 215 HUMAN Phe Met Lys Ile Cys Val Phe Ile Phe Ala Phe Val Ile Pro Val Leu Phe Met Lys Ile Cys Val Phe Val Phe Ala Phe Val Ile Pro Val Leu MOUSE 225 230 Ile Ile Ile Val Cys Tyr Thr Leu Met Ile Leu Arg Leu Lys NNN Val Ile Ile Ile Val Cys Tyr Thr Leu Met Ile Leu Arg Leu Lys Ser Val HUMAN MOUSE

	uman Ouse	Arg Arg	Leu Leu	Leu Leu	Ser 260	Gly Gly	Ser Ser	Arg Arg	Glu Glu	Lys Lys 265	Asp	NNN Arg	As. Asn	Leu Leu	Arg Arg 270	Arg Arg	Ile Ile	80	455(683
	uman Ouse	Thr Thr	Arg Lys	Leu Leu 275	Val Val	Leu Leu	Val Val	Val Val	Val Val 280	Ala Ala	Val Val	Phe Phe	Val Íle	Val Ile 285	Сув Сув	Trp	Thr Thr			
	UMAN OUSE	Pro Pro	Ile Ile 290	His His	Ile Ile	Phe Phe	Ile Ile	Leu Leu 295	Val Val	Glu Glu	Ala Ala	Leu Leu	Gly Gly 300	Ser Ser	Thr Thr	Ser Ser	His His			
	UMAN OUSE	Ser Ser 305	Thr Thr	Ala Ala	Ala Ala	Leu Leu	Ser Ser 310	Ser Ser	Tyr Tyr	Tyr Tyr	Phe Phe	Cys Cys 315	Ile Ile	Ala Ala	Leu Leu	Gly Gly	Tyr Tyr 320			
	UMAN OUSE	Thr Thr	Asn Asn	Ser Ser	Ser Ser	Leu Leu 325	Asn Asn	Pro Pro	Ile Val	Leu Leu	Tyr Tyr 330	Ala Ala	Phe Phe	Leu Leu	Asp Asp	Glu Glu 335	Asn Asn			
HI M	UMAN DUSE	Phe Phe	Lys Lys	Arg Arg	Cys Cys 340	Phe Phe	Arg Arg	Asp Asp	Phe Phe	Cys Cys 345	Phe Phe	Pro Pro	Leu Ile	Lys Lys	Met Met 350	NNN Arg	Met Met			
	JMAN DUSE	Glu Glu	Arg Arg	NNN Gln 355	Ser Ser	Thr Thr	Ser Asn	Arg Arg	Val Val 360	Arg Arg	Asn Asn	Thr Thr	Val Val	Gln Gln 365	Asp	Pro Pro	Ala Ala			
	JMAN DUSE	Tyr	Leu Ser	Arg Met 370	Glu Arg	Ile Asp	Asp Val	Gly Gly	Met Gly 375	Met Met	Asn Asn	Lys Lys	Pro Pro	Val Val 380			ID NO:			

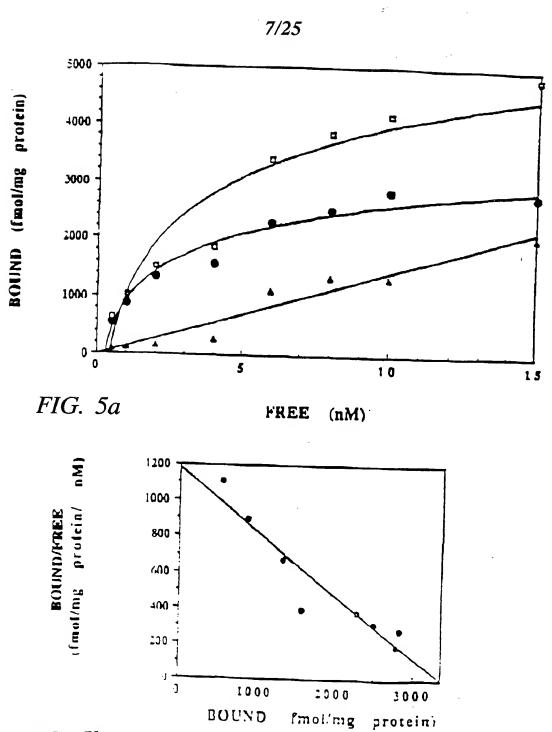


FIG. 5b

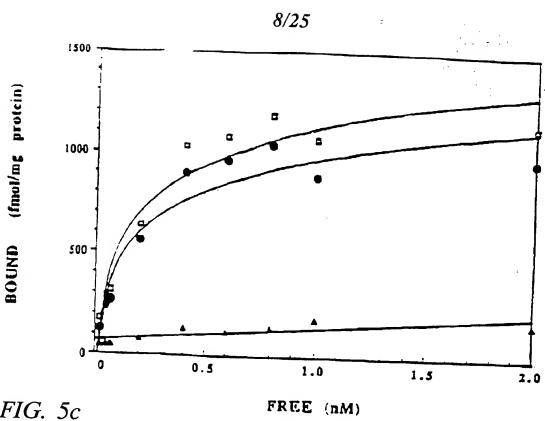


FIG. 5c

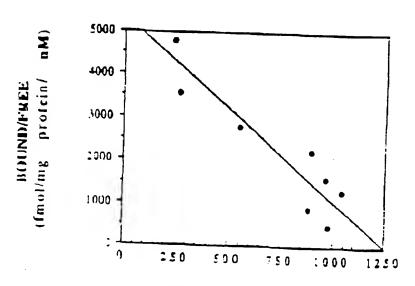
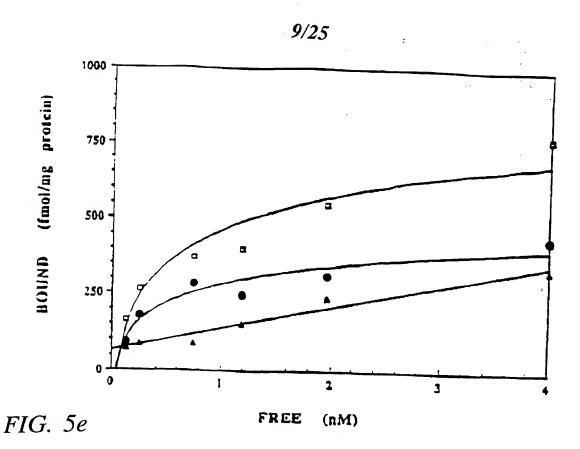
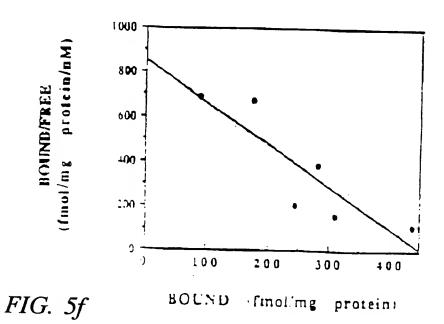


FIG. 5d

BOUND fmol/mg proteini





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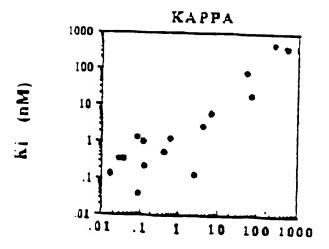


FIG. 6a

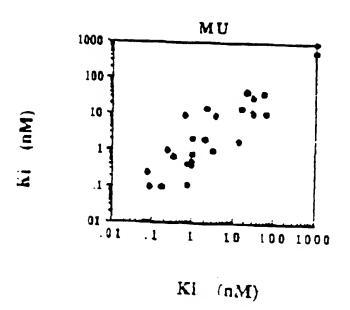
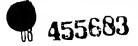


FIG. 6b



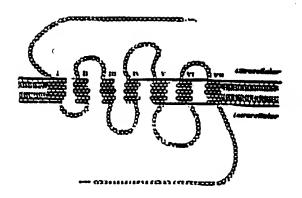


FIG. 7a

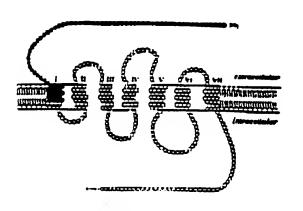


FIG. 7c

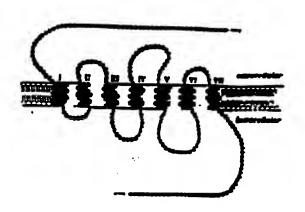


FIG. 7b

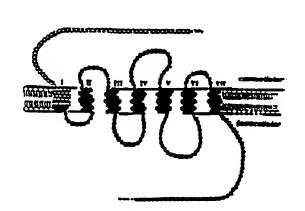


FIG. 7d



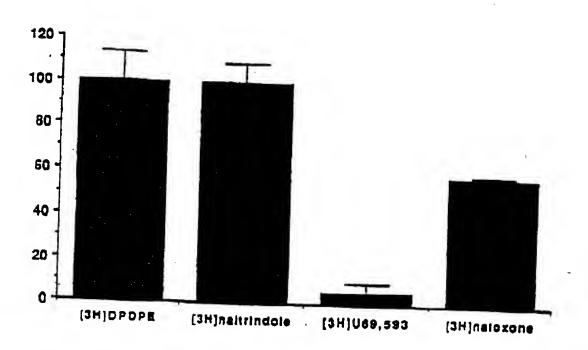


FIG. 8

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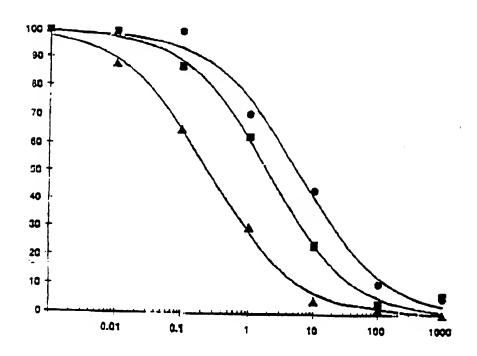


FIG. 9a



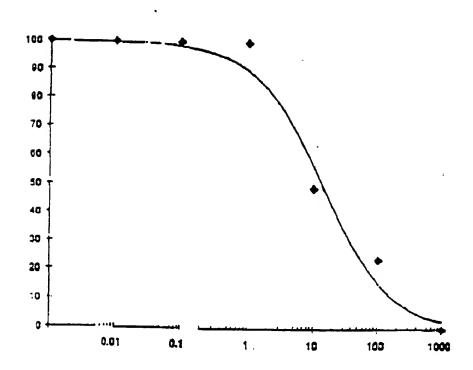


FIG. 9b

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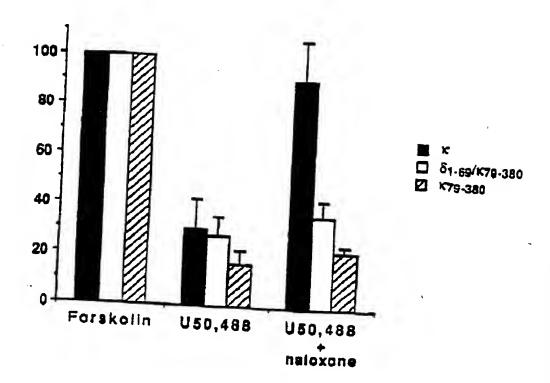


FIG. 10a

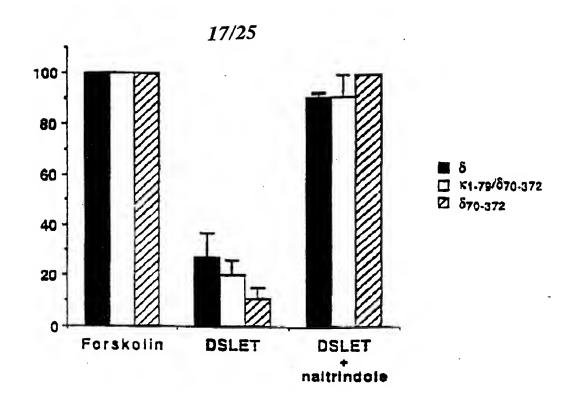


FIG. 10b

1.0

0.5

0.0

1.5

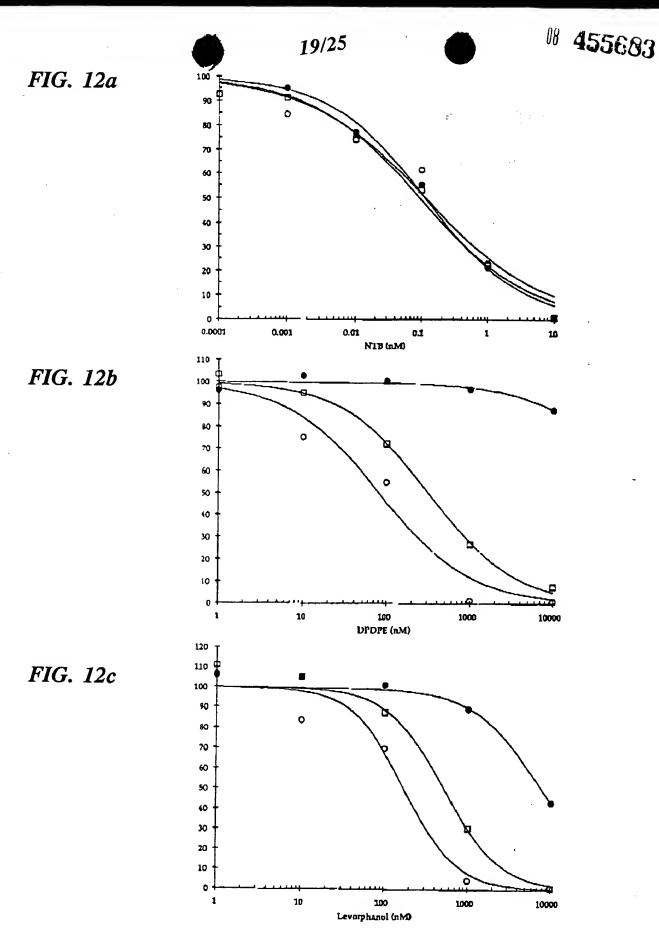
2.0

2.5

3.0

3.5

4.0



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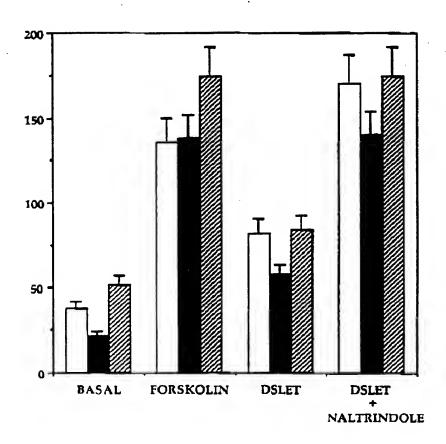
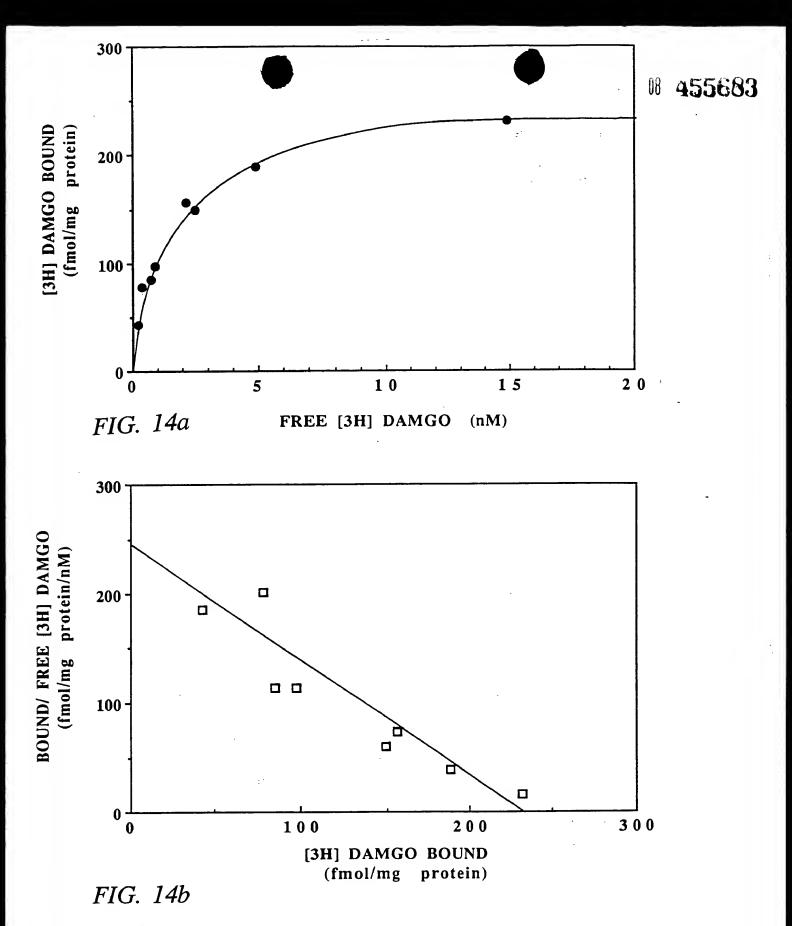
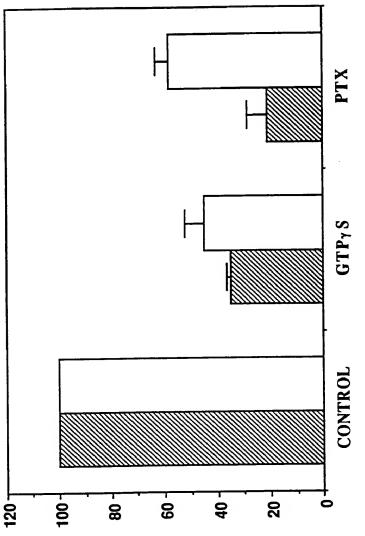
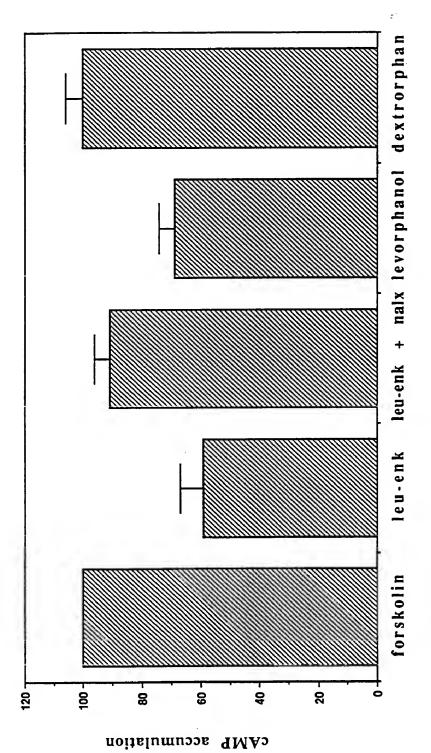


FIG. 13



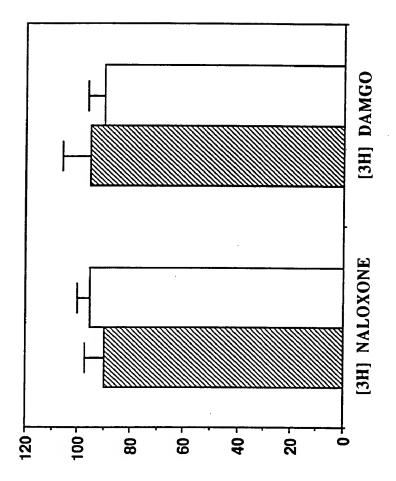


(% CONTROL)
(% DAMGO BINDING



Percent forskolin-stimulated

FIG. 16



(% CONTROL)

KADIOLIGAND BINDING

FIG. 17



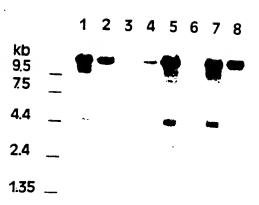


FIG. 18